

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWVDVGDVDAAPLG  
AAPTPGIFSFQPESNPTPAVHRDMAARTSPLRPIVATTGPT  
LSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA  
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS  
PLVDNIALWMTEYLNRLHTWIQDNGGWDAFVELYGPSVRP  
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ  
ID NO: 1)

**FIG. 1**

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWVDVGDVDA**AAA**  
**A**SPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA  
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS  
PLVDNIALWMTEYLNRLHTWIQDNGGWDAFVELYGPSVRP  
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ  
ID NO: 2)

**FIG. 2**

1 ATGGCTCAAG CTGGGAGAAC AGGGTATGAT AACCGAGAGA TCGTGATGAA  
51 GTACATCCAT TATAAGCTGT CACAGAGGGG CTACGAGTGG GATGTGGGAG  
101 ATGTGGACGC CGCGGCCGCG GCCGCGAGCC CCGTGCCACC TGTGGTCCAC  
151 CTGACCCTCC GCCGGGCTGG GGATGACTTC TCCCGTCGCT ACCGTCGCGA  
201 CTTCGCGGAG ATGTCCAGTC AGCTGCACCT GACGCCCTTC ACCGCGAGGG  
251 GACGCTTTGC TACGGTGGTG GAGGAACTCT TCAGGGATGG GGTGAACTGG  
301 GGGAGGATTG TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG  
351 CGTCAACAGG GAGATGTCAC CCCTGGTGGA CAACATCGCC CTGTGGATGA  
401 CCGAGTACCT GAACCGGCAT CTGCACACCT GGATCCAGGA TAACGGAGGC  
451 TGGGACGCAT TTGTGGAACT GTACGGCCCC AGTGTGAGGC CTCTGTTTGA  
501 TTTCTCTTGG CTGTCTCTGA AGACCCTGCT CAGCCTGGCC CTGGTCGGGG  
551 CCTGCATCAC TCTGGGTACC TACCTGGGCC ACAAGTGA (SEQ ID NO: 3)

**FIG. 3**

MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFE  
PPTLHELHDLDVTAPEDPNEEA VSQIFPDSVMLAVQEGI  
DLLTFPPAPGSPEPPHLSRQPEQPEQRALGPVSMPNLVP  
EVIDLTGHEAGFPSPDDEDEEGEEFVLDYVEHPGHGCR  
SCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPE  
PEPEPEPARPTRRPKMAPAILRRPTSPVSRECNSSTDSCD  
SGPSNTPPEIHPVVPLCPIKPVA VRVGGRRQAVECIEDL  
LNEPGQPLDL SCKRPRP (SEQ ID NO: 4)

FIG. 4

1 ATGAGACATA TTATCTGCCA CGGAGGTGTT ATTACCGAAG AAATGGCCGC  
51 CAGTCTTTTG GACCAGCTGA TCGAAGAGGT ACTGGCTGAT AATCTTCCAC  
101 CTCCTAGCCA TTTTGAACCA CCTACCCTTC ACGAACTGCA TGATTTAGAC  
151 GTGACGGCCC CCGAAGATCC CAACGAGGAG GCGGTTTCGC AGATTTTTC  
201 CGACTCTGTA ATGTTGGCGG TGCAGGAAGG GATTGACTTA CTCACTTTTC  
251 CGCCGGCGCC CGGTTCTCCG GAGCCGCCTC ACCTTTCCCG GCAGCCCGAG  
301 CAGCCGGAGC AGAGAGCCTT GGGTCCGGTT TCTATGCCAA ACCTTGTAAC  
351 GGAGGTGATC GATCTTACCG GCCACGAGGC TGGCTTTCCA CCCAGTGACG  
401 ACGAGGATGA AGAGGGTGAG GAGTTTGTGT TAGATTATGT GGAGCACCCC  
451 GGGCACGGTT GCAGGTCTTG TCATTATCAC CGGAGGAATA CGGGGGACCC  
501 AGATATTATG TGTTGCTTTT GCTATATGAG GACCTGTGGC ATGTTTGTCT  
551 ACAGTAAGTG AAAATTATGG GCAGTGGGTG ATAGAGTGGT GGGTTTGGTG  
601 TGGTAATTTT TTTTTTAATT TTTACAGTTT TGTGGTTTAA AGAATTTTGT  
651 ATTGTGATTT TTTTAAAAGG TCCTGTGTCT GAACCTGAGC CTGAGCCCGA  
701 GCCAGAACCG GAGCCTGCAA GACCTACCCG CCGTCCTAAA ATGGCGCCTG  
751 CTATCCTGAG ACGCCCGACA TCACCTGTGT CTAGAGAATG CAATAGTAGT  
801 ACGGATAGCT GTGACTCCGG TCCTTCTAAC ACACCTCCTG AGATACACCC  
851 GGTGGTCCCG CTGTGCCCCA TTAAACCAGT TGCCGTGAGA GTTGGTGGGC  
901 GTCGCCAGGC TGTGGAATGT ATCGAGGACT TGCTTAACGA GCCTGGGCAA  
951 CCTTTGGACT TGAGCTGTAA ACGCCCCAGG CCATAA (SEQ ID NO: 5)

FIG. 5

1 GAATTCGCCG CCACCATGGA GGCTTGGGAG TGTTTGGAAG ATTTTCTGC  
51 TGTGCGTAAC TTGCTGGAAC AGAGCTCTAA CAGTACCTCT TGGTTTGGGA  
101 GGTTTCTGTG GGGCTCATCC CAGGCAAAGT TAGTCTGCAG AATTAAGGAG  
151 GATTACAAGT GGAATTTGA AGAGCTTTTG AAATCCTGTG GTGAGCTGTT  
201 TGATTCTTTG AATCTGGGTC ACCAGGCGCT TTTCCAAGAG AAGGTCATCA  
251 AGACTTTGGA TTTTCCACA CCGGGGCGCG CTGCGGCTGC TGTGCTTTT  
301 TTGAGTTTTA TAAAGGATAA ATGGAGCGAA GAAACCCATC TGAGCGGGGG  
351 GTACCTGCTG GATTTTCTGG CCATGCATCT GTGGAGAGCG GTTGTGAGAC  
401 ACAAGAATCG CCTGCTACTG TTGTCTTCCG TCCGCCCggc GATAATACCG  
451 ACGGAGGAGC AGCAGCAGCA GCAGGAGGAA GCCAGGCGGC GCGGCAGGA  
501 GCAGAGCCCA TGAACCCGA GAGCCGGCCT GGACCCTCGG GAATGAATGT  
551 TGGTCGAC (SEQ ID NO: 15)

FIG. 6

SalI

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1  GTCGACGCCG  CCACCATGCC  GCCCAAAACC  CCCCAGAAAA  CGGCCGCCAC
      M  P      P  K  T      P  R  K  T      A  A  T

51  CGCCGCCGCT  GCCGCCGCGG  AACCCCCGGC  ACCGCCGCCG  CCGCCCCCTC
      A  A  A      A  A  A  E      P  P  A      P  P  P      P  P  P  P

101 CTGAGGAGGA  CCCAGAGCAG  GACAGCGGCC  CGGAGGACCT  GCCTCTCGTC
      E  E  D      P  E  Q      D  S  G  P      E  D  L      P  L  V

151 AGGCTTGAGT  TTGAAGAAAC  AGAAGAACCT  GATTTTACTG  CATTATGTCA
      R  L  E  F      E  E  T      E  E  P      D  F  T  A      L  C  Q

201 GAAATTAAAG  ATACCAGATC  ATGTCAGAGA  GAGAGCTTGG  TTAAGTTGGG
      K  L  K      I  P  D  H      V  R  E      R  A  W      L  T  W  E

251 AGAAAGTTTC  ATCTGTGGAT  GGAGTATTGG  GAGGTTATAT  TCAAAAGAAA
      K  V  S      S  V  D      G  V  L  G      G  Y  I      Q  K  K

301 AAGGAACTGT  GGGGAATCTG  TATCTTTATT  GCACGAGTTG  ACCTAGATGA
      K  E  L  W      G  I  C      I  F  I      A  R  V  D      L  D  E

351 GATGTCGTTC  ACTTTACTGA  GCTACAGAAA  AACATACGAA  ATCAGTGTCC
      M  S  F      T  L  L  S      Y  R  K      T  Y  E      I  S  V  H

401 ATAAATTCTT  TAACTTACTA  AAAGAAATTG  ATACCAGTAC  CAAAGTTGAT
      K  F  F      N  L  L      K  E  I  D      T  S  T      K  V  D

451 AATGCTATGT  CAAGACTGTT  GAAGAAGTAT  GATGTATTGT  TTGCACTCTT
      N  A  M  S      R  L  L      K  K  Y      D  V  L  F      A  L  F

501 CAGCAAATTG  GAAAGGACAT  GTGAACTTAT  ATATTTGACA  CAACCCAGCA
      S  K  L      E  R  T  C      E  L  I      Y  L  T      Q  P  S  S

551 GTTCGATATC  TACTGAAATA  AATTCTGCAT  TGGTGCTAAA  AGTTTCTTGG
      S  I  S      T  E  I      N  S  A  L      V  L  K      V  S  W

601 ATCACATTTT  TATTAGCTAA  AGGGGAAGTA  TTACAAATGG  AAGATGATCT
      I  T  F  L      L  A  K      G  E  V      L  Q  M  E      D  D  L

651 GGTGATTTCA  TTTCAGTTAA  TGCTATGTGT  CCTTGACTAT  TTTATTAAAC
      V  I  S      F  Q  L  M      L  C  V      L  D  Y      F  I  K  L

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FIG. 7A

701 TCTCACCTCC CATGTTGCTC AAAGAACCAT ATAAAACAGC TGTTATACCC  
S P P M L L K E P Y K T A V I P

751 ATTAATGGTT CACCTCGAAC ACCCAGGCGA GGTCAGAACA GGAGTGCACG  
I N G S P R T P R R G Q N R S A R

801 GATAGCAAAA CAACTAGAAA ATGATACAAG AATTATTGAA GTTCTCTGTA  
I A K Q L E N D T R I I E V L C K

851 AAGAACATGA ATGTAATATA GATGAGGTGA AAAATGTTTA TTTCAAAAAT  
E H E C N I D E V K N V Y F K N

EcoRI

901 TTTATACCTT TTATGAATTC TCTTGGA CTT GTAACATCTA ATGGACTTCC  
F I P F M N S L G L V T S N G L P

951 AGAGGTTGAA AATCTTTCTA AACGATACGA AGAAATTTAT CTTAAAAATA  
E V E N L S K R Y E E I Y L K N K

1001 AAGATCTAGA TCGAAGATTA TTTTGGATC ATGATAAAAC TCTTCAGACT  
D L D R R L F L D H D K T L Q T

1051 GATTCTATAG ACAGTTTTGA AACACAGAGA ACACCACGAA AAAGTAACCT  
D S I D S F E T Q R T P R K S N L

1101 TGATGAAGAG GTGAATATAA TTCCTCCACA CACTCCAGTT AGGACTGTTA  
D E E V N I I P P H T P V R T V M

1151 TGAACACTAT CCAACAATTA ATGATGATTT TAAATTCTGC AAGTGATCAA  
N T I Q Q L M M I L N S A S D Q

1201 CCTTCAGAAA ATCTGATTTT CTATTTTAAAC AACTGCACAG TGAATCCAAA  
P S E N L I S Y F N N C T V N P K

1251 AGAAAGTATA CTGAAAAGAG TGAAGGATAT AGGATACATC TTAAAGAGA  
E S I L K R V K D I G Y I F K E K

1301 AATTTGCTAA AGCTGTGGGA CAGGGTTGTG TCGAAATTGG ATCACAGCGA  
F A K A V G Q G C V E I G S Q R

1351 TACAACTTG GAGTTCGCTT GTATTACCGA GTAATGGAAT CCATGCTTAA  
Y K L G V R L Y Y R V M E S M L K

FIG. 7B



1401 ATCAGAAGAA GAACGATTAT CCATTCAAAA TTTTAGCAAA CTTCTGAATG  
S E E E R L S I Q N F S K L L N D

1451 ACAACATTTT TCATATGTCT TTATTGGCGT GCGCTCTTGA GGTTGTAATG  
N I F H M S L L A C A L E V V M

1501 GCCACATATA GCAGAAGTAC ATCTCAGAAT CTTGATTCTG GAACAGATTT  
A T Y S R S T S Q N L D S G T D L

1551 GTCTTTCCCA TGGATTCTGA ATGTGCTTAA TTTAAAAGCC TTTGATTTTT  
S F P W I L N V L N L K A F D F Y

1601 ACAAAGTGAT CGAAAGTTTT ATCAAAGCAG AAGGCAACTT GACAAGAGAA  
K V I E S F I K A E G N L T R E

1651 ATGATAAAAC ATTTAGAACG ATGTGAACAT CGAATCATGG AATCCCTTGC  
M I K H L E R C E H R I M E S L A

1701 ATGGCTCTCA GATTCACCTT TATTTGATCT TATTAAACAA TCAAAGGACC  
W L S D S P L F D L I K Q S K D R

1751 GAGAAGGACC AACTGATCAC CTTGAATCTG CTTGTCCTCT TAATCTTCCT  
E G P T D H L E S A C P L N L P

1801 CTCCAGAATA ATCACACTGC AGCAGATATG TATCTTTCTC CTGTAAGATC  
L Q N N H T A A D M Y L S P V R S

1851 TCCAAAGAAA AAAGGTTCAA CTACGCGTGT AAATTCTACT GCAAATGCAG  
P K K K G S T T R V N S T A N A E

1901 AGACACAAGC AACCTCAGCC TTCCAGACCC AGAAGCCATT GAAATCTACC  
T Q A T S A F Q T Q K P L K S T

1951 TCTCTTTCAC TGTTTTATAA AAAAGTGTAT CGGCTAGCCT ATCTCCGGCT  
S L S L F Y K K V Y R L A Y L R L

2001 AAATACACTT TGTGAACGCC TTCTGTCTGA GCACCCAGAA TTAGAACATA  
N T L C E R L L S E H P E L E H I

2051 TCATCTGGAC CCTTTTCCAG CACACCCTGC AGAATGAGTA TGAACTCATG  
I W T L F Q H T L Q N E Y E L M

FIG. 7C

2101 AGAGACAGGC ATTTGGACCA AATTATGATG TGTTCATGT ATGGCATATG  
R D R H L D Q I M M C S M Y G I C

2151 CAAAGTGAAG AATATAGACC TTAAATTCAA AATCATTGTA ACAGCATACA  
K V K N I D L K F K I I V T A Y K

2201 AGGATCTTCC TCATGCTGTT CAGGAGACAT TCAAACGTGT TTTGATCAAA  
D L P H A V Q E T F K R V L I K

2251 GAAGAGGAGT ATGATTCTAT TATAGTATTC TATAACTCGG TCTTCATGCA  
E E E Y D S I I V F Y N S V F M Q

2301 GAGACTGAAA ACAAATATTT TGCAGTATGC TTCCACCAGG CCCCTACCT  
R L K T N I L Q Y A S T R P P T L

2351 TGTCACCAAT ACCTCACATT CCTCGAAGCC CTTACAAGTT TCCTAGTTCA  
S P I P H I P R S P Y K F P S S

2401 CCCTTACGGA TTCCTGGAGG GAACATCTAT ATTTACCCCC TGAAGAGTCC  
P L R I P G G N I Y I S P L K S P

2451 ATATAAAATT TCAGAAGGTC TGCCAACACC AACAAAAATG ACTCCAAGAT  
Y K I S E G L P T P T K M T P R S

2501 CAAGAATCTT AGTATCAATT GGTGAATCAT TCGGGACTTC TGAGAAGTTC  
R I L V S I G E S F G T S E K F

2551 CAGAAAATAA ATCAGATGGT ATGTAACAGC GACCGTGTGC TCAAAAGAAG  
Q K I N Q M V C N S D R V L K R S

2601 TGCTGAAGGA AGCAACCCTC CTAAACCACT GAAAAAACTA CGCTTTGATA  
A E G S N P P K P L K K L R F D I

2651 TTGAAGGATC AGATGAAGCA GATGGAAGTA AACATCTCCC AGGAGAGTCC  
E G S D E A D G S K H L P G E S

2701 AAATTTTCAGC AGAAACTGGC AGAAATGACT TCTACTCGAA CACGAATGCA  
K F Q Q K L A E M T S T R T R M Q

2751 AAAGCAGAAA ATGAATGATA GCATGGATAC CTCAAACAAG GAAGAGAAAT  
K Q K M N D S M D T S N K E E K \*

NotI

2801 GAGGATCTCA GGACCGGCGG CCGC

FIG. 7D

EcoRI

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1 GAATTCGCCG CCACCATGAC CATGGACTCT GGAGCAGACA ACCAGCAGAG
      M T M D S G A D N Q Q S

51 TGGAGATGCA GCTGTAACAG AAGCTGAAAA CCAACAAATG ACAGTTCAAG
      G D A A V T E A E N Q Q M T V Q A

101 CCCAGCCACA GATTGCCACA TTAGCCCAGG TATCTATGCC AGCAGCTCAT
      Q P Q I A T L A Q V S M P A A H

151 GCAACATCAT CTGCTCCAC CGTAACTCTA GTACAGCTGC CCAATGGGCA
      A T S S A P T V T L V Q L P N G Q

201 GACAGTTCAA GTCCATGGAG TCATTCAGGC GGCCCAGCCA TCAGTTATTC
      T V Q V H G V I Q A A Q P S V I Q

251 AGTCTCCACA AGTCCAAACA GTTCAGATTT CAACTATTGC AGAAAGTGAA
      S P Q V Q T V Q I S T I A E S E

301 GATTCACAGG AGTCAGTGGA TAGTGTA ACT GATTCCCAA AGCGAAGGGA
      D S Q E S V D S V T D S Q K R R E

351 AATTCTTTCA AGGAGGCCTT CCTTCAGGAA AATTTTGAAT GACTTATCTT
      I L S R R P S F R K I L N D L S S

401 CTGATGCACC AGGAGTGCCA AGGATTGAAG AAGAGAAGTC TGAAGAGGAG
      D A P G V P R I E E E K S E E E

451 GCTTCAGCAC CTGCCATCAC CGCTGTAGCG GTGCCAACGC CAATTTACCG
      A S A P A I T A V A V P T P I Y R

501 GACTAGCAGT GGACAGTATA TTACCATTAC CCAGAGAGGA GCAATACAGC
      T S S G Q Y I T I T Q R G A I Q L

551 TGGCTAGCAA TGGTACCGAT GGGGTACAGG GCCTGCAAAC ATTAACCATG
      A S N G T D G V Q G L Q T L T M

601 GCCAATGCAG CAGCCACTCA GCCGGGTACT ACCATTCTAC AGTATGCACA
      A N A A A T Q P G T T I L Q Y A Q

651 GACCACTGAT GGACAGCAGA TCTTAGTGCC CAGCAACCAA GTTGTGTGTC
      T T D G Q Q I L V P S N Q V V V Q

```

FIG. 8A

701 AAGCTGCCTC TGGAGACGTA CAAACATACC AGATTCGCAC AGCACCCACT  
A A S G D V Q T Y Q I R T A P T

751 AGCACTATTG CCCCTGGAGT TGTTATGGCA TCCTCCCCAG CACTTCCTAC  
S T I A P G V V M A S S P A L P T

801 ACAGCCTGCT GAAGAAGCAG CACGAAAGAG AGAGGTCCGT CTAATGAAGA  
Q P A E E A A R K R E V R L M K N

851 ACAGGGAAGC AGCTCGTGAG TGTCGTAGAA AGAAGAAAGA ATATGTGAAA  
R E A A R E C R R K K K E Y V K

901 TGTTTAGAAA ACAGAGTGGC AGTGCTTGAA AATCAAAACA AGACATTGAT  
C L E N R V A V L E N Q N K T L I

951 TGAGGAGCTA AAAGCACTTA AGGACCTTTA CTGCCACAAA TCAGATTAAT  
E E L K A L K D L Y C H K S D \*

Sali

1001 TTGGGTCGAC

FIG. 8B



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1  aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
   HindIII      M R H I I C H G G V I
51  cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
   T E E M A A S L L D Q L I E E V L
101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
   A D N L P P P S H F E P P T L H E
151 ctgtatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcggt
   L Y D L D V T A P E D P N E E A
201 ttgcgagatt tttcccgact ctgtaatggt ggcggtgcag gaagggattg
   V S Q I F P D S V M L A V Q E G I
251 acttactcac ttttccgccg gcgccccggt ctccggagcc gcctcacctt
   D L L T F P P A P G S P E P P H L
301 tcccggcagc ccgagcagcc ggagcagaga gccttggttc cggtttctat
   S R Q P E Q P E Q R A L G P V S
351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
   M P N L V P E V I D L T C H E A G
401 ttccaccagc tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
   F P P S D D E D E E G E E F V L D
451 tatgtggagc accccgggca cgggtgcagg tcttgtcatt atcaccggag
   Y V E H P G H G C R S C H Y H R
501 gaatacgggg gaccagata ttatgtgttc gctttgctat atgaggacct
   R N T G D P D I M C S L C Y M R T
551 gtggcatggt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
   C G M F V Y S P V S E P E P E P E
601 ccagaaccgg agcctgcaag acctaccgc cgtcctaaaa tggcgccctgc
   P E P E P A R P T R R P K M A P
651 taccctgaga cgcccacat cacctgtgtc tagagaatgc aatagtagta
   A I L R R P T S P V S R E C N S S
701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
   T D S C D S G P S N T P P E I H P
751 gtggtccgcg tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
   V V P L C P I K P V A V R V G G
801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
   R R Q A V E C I E D L L N E P G Q
851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
   P L D L S C K R P R P - XhoI

```

**Figure 10. Nucleotide coding sequence of E1a cDNA (SEQ ID NO: 40). Cloning sites HindIII and XhoI, and two amino acid residue positions Y47 and C124 are underscored.**

```

1  aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
   HindIII           M R H I I C H G G V I
51  cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
   T E E M A A S L L D Q L I E E V L
101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
   A D N L P P P S H F E P P T L H E
151 ctgcatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcggg
   L H D L D V T A P E D P N E E A
201 ttcgcagatt tttcccgaact ctgtaatggt ggcggtgcag gaagggattg
   V S Q I F P D S V M L A V Q E G I
251 acttactcac ttttccgccg gcgcccgggt ctccggagcc gcctcacctt
   D L L T F P P A P G S P E P P H L
301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
   S R Q P E Q P E Q R A L G P V S
351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
   M P N L V P E V I D L T C H E A G
401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
   F P P S D D E D E E G E E F V L D
451 tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
   Y V E H P G H G C R S C H Y H R
501 gaatacgggg gaccagata ttatgtgttc gctttgctat atgaggacct
   R N T G D P D I M C S L C Y M R T
551 gtggcatggt tgtctacagt cctgtgtctg aacctgagcc tgagcccag
   C G M F V Y S P V S E P E P E P E
601 ccagaaccgg agcctgcaag acctaccgcg cgtcctaaaa tggcgccctgc
   P E P E P A R P T R R P K M A P
651 tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
   A I L R R P T S P V S R E C N S S
701 cggatagctg tgactccggg ccttctaaca cacctcctga gatacacccg
   T D S C D S G P S N T P P E I H P
751 gtgggtccgc tgtgccccat taaaccagtt gccgtgagag ttgggtgggcg
   V V P L C P I K P V A V R V G G
801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
   R R Q A V E C I E D L L N E P G Q
851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
   P L D L S C K R P R P - XhoI

```

**Figure 11. Nucleotide coding sequence of E1a\_Y47H (SEQ ID NO: 41). Cloning sites HindIII and XhoI are underscored.**

```

1  aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
   HindIII      M T M E S G A D N Q Q
51  tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
   S G D A A V T E A E N Q Q M T A Q
101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
   A Q P Q I A T L A Q V S M P A A H
151 gcgacatcat ctgctccac tgtaacctta gtgcagctgc ccaatgggca
   A T S S A P T V T L V Q L P N G
201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
   Q T V Q V H G V I Q A A Q P S V I
251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
   Q S P Q V Q T V Q S S C K D L K R
301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
   L F S G T Q I S T I A E S E D S
351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
   Q E S V D S V T D S Q K R R E I L
401 caaggaggcc ttcctacagg aaaattttga atgacttatc ttctgatgca
   S R R P S Y R K I L N D L S S D A
451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
   P G V P R I E E E K S E E E T S
501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
   A P A I T T V T V P T P I Y Q T S
551 gtgggcagta tattgccatt acccaggagg gagctataca gctggctaac
   S G Q Y I A I T Q G G A I Q L A N
601 aatgggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
   N G T D G V Q G L Q T L T M T N
651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
   A A A T Q P G T T I L Q Y A Q T T
701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
   D G Q Q I L V P S N Q V V V Q A A
751 tctggcgatg taaaaacata ccaaattcgt acagcaccca ctagcaccat
   S G D V Q T Y Q I R T A P T S T
801 cgccccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
   I A P G V V M A S S P A L P T Q P
851 ctgaagaagc agcccggaag agagagggtc gtctaataaa gaacagggaa
   A E E A A R K R E V R L M K N R E
901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
   A A R E C R R K K K E Y V K C L
951 gaacagagtg gcagtgcctg aaaacaaaa caagacattg attgaggagc
   E N R V A V L E N Q N K T L I E E
1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
   L K A L K D L Y C H K S D - BamHI

```

**Figure 12. Nucleotide coding sequence of hamster CREB-B cDNA (SEQ ID NO: 42).**

Cloning sites HindIII and BamHI are underscored.



```

1  aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
   HindIII           M T M E S G A D N Q Q
51  tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
   S G D A A V T E A E N Q Q M T A Q
101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
   A Q P Q I A T L A Q V S M P A A H
151 gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
   A T S S A P T V T L V Q L P N G
201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
   Q T V Q V H G V I Q A A Q P S V I
251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
   Q S P Q V Q T V Q S S C K D L K R
301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
   L F S G T Q I S T I A E S E D S
351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
   Q E S V D S V T D S Q K R R E I L
401 caaggaggcc ttcctccagg aaaattttga atgacttattc ttctgatgca
   S R R P S F R K I L N D L S S D A
451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
   P G V P R I E E E K S E E E T S
501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
   A P A I T T V T V P T F I Y Q T S
551 gtgggcagta tattgccatt acccaggagg gagctataca gctggctaac
   S G Q Y I A I T Q G G A I Q L A N
601 aatgggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
   N G T D G V Q G L Q T L T M T N
651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
   A A A T Q P G T T I L Q Y A Q T T
701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
   D G Q Q I L V P S N Q V V V Q A A
751 tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
   S G D V Q T Y Q I R T A P T S T
801 cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
   I A P G V V M A S S P A L P T Q P
851 ctgaagaagc agcccgggaag agagagggttc gtctaataaa gaacagggaa
   A E E A C R K R E V R L M K N R E
901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
   A A R E C R R K K K E Y V K C L
951 gaacagagtg gcagtgcctg aaaacaaaaa caagacattg attgaggagc
   E N R V A V L E N Q N K T L I E E
1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
      L K A L K D L Y C H K S D - BamHI

```

**Figure 13. Nucleotide coding sequence of hamster CREB-B Y134F cDNA (SEQ ID NO: 43). Cloning sites HindIII and BamHI are underscored.**

```

1  aagcttactg ttggtaaagc cgccaccatg gaggcttggg agtgtttggg
   HindIII                               M   E   A   W   E   C   L

51  agatttttct gctgtgcgta acttgctgga acagagctct aacagtacct
   E   D   F   S   A   V   R   N   L   L   E   Q   S   S   N   S   T

101 cttgggttttg gaggtttctg tggggctcat cccaggcaaa gttagtctgc
    S   W   F   W   R   F   L   W   G   S   S   Q   A   K   L   V   C

151 agaattaagg aggattacaa gtgggaattt gaagagcttt tgaaatcctg
    R   I   K   E   D   Y   K   W   E   F   E   E   L   L   K   S

201 tggtgagctg tttgattctt tgaatctggg tcaccaggcg cttttccaag
    C   G   E   L   F   D   S   L   N   L   G   H   Q   A   L   F   Q

251 agaaggtcac caagactttg gatttttcca caccggggcg cgctgcggct
    E   K   V   I   K   T   L   D   F   S   T   P   G   R   A   A   A

301 gctgttgctt ttttgagttt tataaaggat aaatggagcg aagaaaccca
    A   V   A   F   L   S   F   I   K   D   K   W   S   E   E   T

351 tctgagcggg gggtagctgc tggattttct ggccatgcat ctgtggagag
    H   L   S   G   G   Y   L   L   D   F   L   A   M   H   L   W   R

401 cggttgtgag acacaagaat cgcctgctac tgttgtcttc cgtccgcccc
    A   V   V   R   H   K   N   R   L   L   L   L   S   S   V   R   P

451 gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg
    A   I   I   P   T   E   E   Q   Q   Q   Q   Q   E   E   A   R

501 gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc
    R   R   R   Q   E   Q   S   P   W   N   P   R   A   G   L   D   P

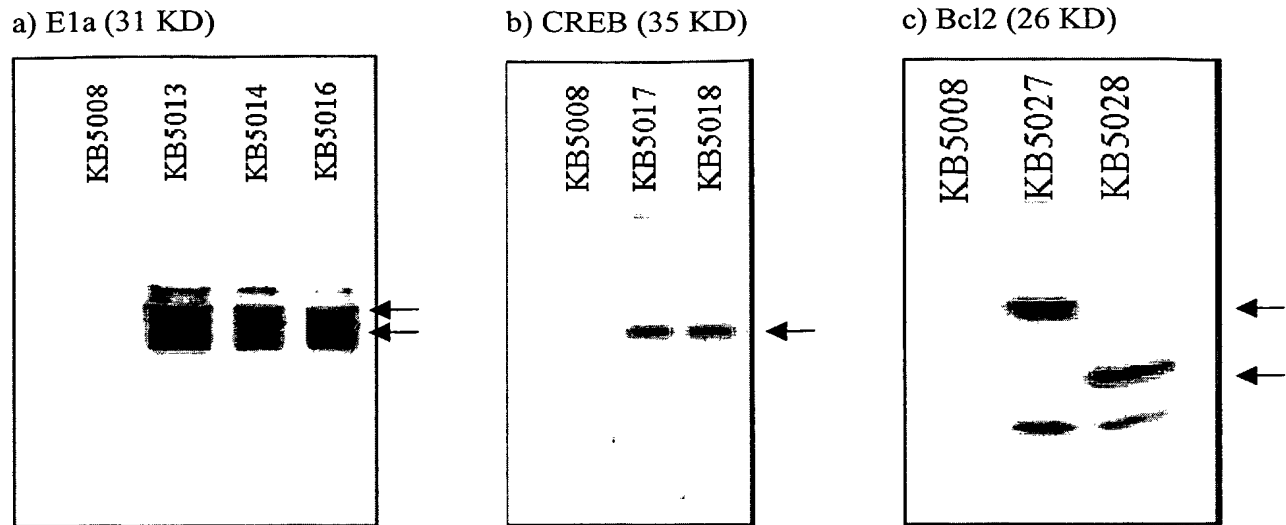
551 gggaatgatc taga
    R   E   -   XbaI

```

**Figure 14. Nucleotide coding sequence of E1b-19K (SEQ ID NO: 44). Cloning sites HindIII and XbaI are underscored.**

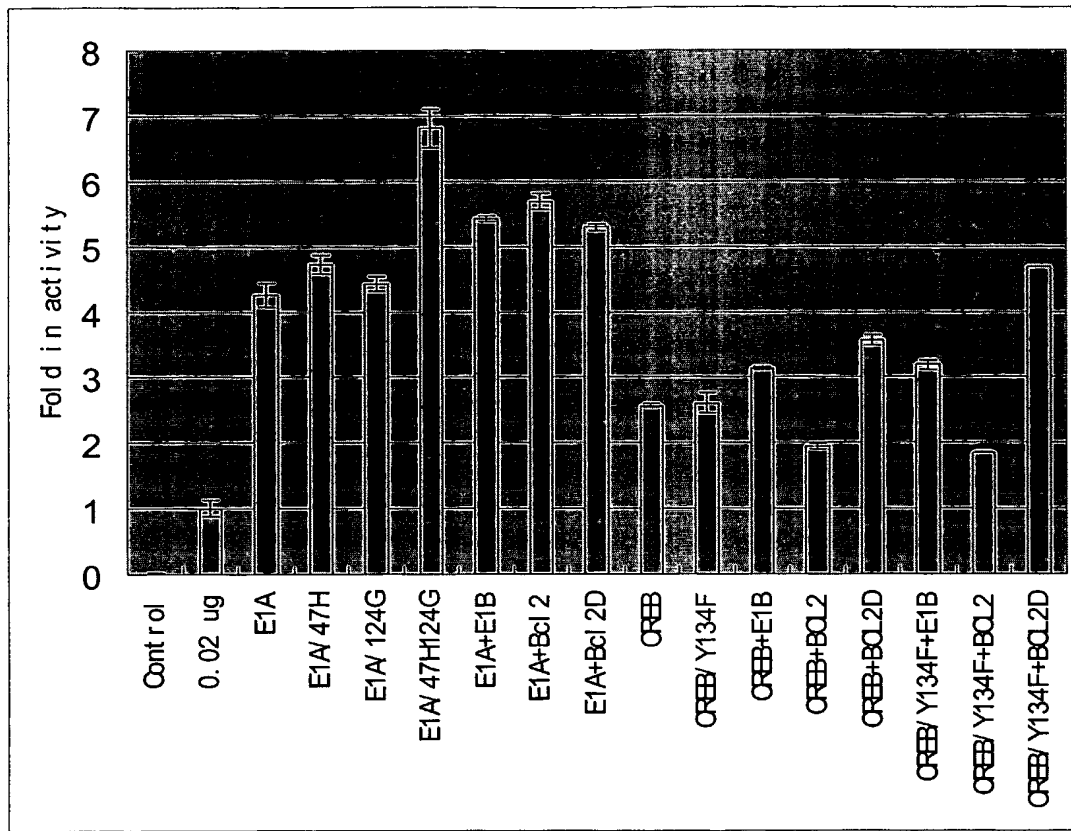
*NcoI*  
 1 ccatgggtcaca agctgggaga acaggggtatg ataaccgaga gatcgtgatg  
    M A Q A G R T G Y D N R E I V M  
 51 aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg  
    K Y I H Y K L S Q R G Y E W D V  
 101 agatgtggac gccgcggccg cggccgcgag ccccggtgcca cctgtggtcc  
    G D V D A A A A A A S P V P P V V  
 151 acctgaccct ccgcccggct ggggatgact tctcccgtcg ctaccgtcgc  
    H L T L R R R A G D D F S R R Y R R  
 201 gacttcgcgg agatgtccag tcagctgcac ctgacgccct tcaccgcgag  
    D F A E M S S Q L H L T P F T A  
 251 gggacgcttt gctacgggtg tggaggaact cttcagggat ggggtgaact  
    R G R F A T V V E E L F R D G V N  
 301 gggggaggat tgtggccttc tttgagttcg gtgggggtcat gtgtgtggag  
    W G R I V A F F E F G G V M C V E  
 351 agcgtcaaca gggagatgtc acccctggtg gacaacatcg ccctgtggat  
    S V N R E M S P L V D N I A L W  
 401 gaccgagtac ctgaaccggc atctgcacac ctggatccag gataacggag  
    M T E Y L N R H L H T W I Q D N G  
 451 gctgggacgc atttgtggaa ctgtacggcc ccagtgtgag gcctctgttt  
    G W D A F V E L Y G P S V R P L F  
 501 gatttctctt ggctgtctct gaagaccctg ctcagcctgg ccctgggtcgg  
    D F S W L S L K T L L S L A L V  
 551 ggccctgcatc actctgggta cctacctggg ccacaagtga tctaga  
    G A C I T L G T Y L G H K - XbaI

**Figure 15. Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45). Cloning sites NcoI and XbaI are underscored.**



**Figure 16. Western blots of E1a, CREB and Bcl2.**

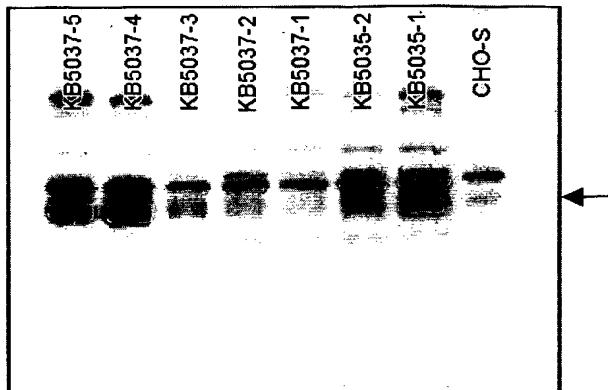
In a), b), and c),  $1 \times 10^5$  CHO-K1 cells were transfected with 0.4  $\mu$ g of indicated plasmid DNA. Cell lysates were collected after 48 hours and probed with appropriate antibodies. KB5008 transfected cells were used as negative controls.



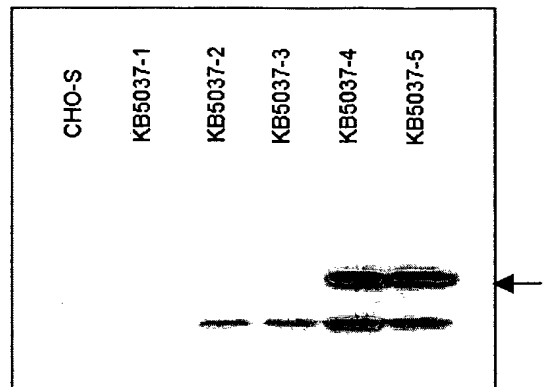
**Figure 17. E1a and CREB enhanced CMV promoter in CHO-K1 cells.**

$1 \times 10^5$  cells were transfected with 0.02  $\mu\text{g}$  of SEAP reporter construct KB5019 and 0.2  $\mu\text{g}$  of E1a or CREB expressing constructs. Total DNA was added up to 0.4  $\mu\text{g}/\text{well}$  by control plasmid KB5008, E1b-19K or Bcl2 expressing plasmids. SEAP activities from culture media were assay 48 hours after transfection. The control was mock transfected CHO-K1 cells.

a) CREB (35 KD)



b) Bcl2D (22KD)



**Figure 18. Western blots showing overexpression of hamster CREB-B Y134F and hamster  $\Delta$ Bcl-2 in stable transfectant CHO-S cell lines.**